Nucleotide sequence of the *Borrelia burgdorferi rpmH* gene encoding ribosomal protein L34

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The *rpmH* gene, which encodes the ribosomal protein L34, is located close to the origin of replication (*oriC*) in bacteria such as *Escherichia coli, Pseudomonas aeruginosa, P.putida and Bacillus subtilis* (1). From a *B.burgdorferi* library of chromosomally-enriched DNA (2) we isolated homologues of the closely linked genes *gyrB, gyrA*, and *rpmH*. We have determined the complete nucleotide sequence of the *rpmH* homologue of *B.burgdorferi* strain 212. The putative *B.burgdorferi* L34 polypeptide exhibits 70% identity with that of *Proteus mirabilis* (3) 72% with *Escherichia coli* (4) 58% with *Micrococcus luteus* (5) and 68% identity with the partially sequenced *Mycoplasma capricolum rpmH* gene (6) (Figure 1). This high degree of conservation is probably due to constraints caused by the necessity for L34 to interact with other ribosomal components. The 153 nucleotide open reading frame codes for a polypeptide of 51 amino acids with molecular weight of 6,197 Da. The initiator codon of *rpmH* of *E.coli, M.capricolum* and *P.mirabilis* is ATG while for *Micrococcus luteus* it is GTG. The initiator codon of *B.burdorferi rpmH* appears to be TTG, an inefficient initiator codon (7), which is preceded by a strong ribosome binding site, TGGAGGA. A possible promoter, **TTG-ACA-17N-TACCAT** is located 60 bp upstream of the start codon. The GC% of *B.burgdorferi* is one of the lowest in eubacteria (28−31%) and the codon usage is biased to use A and T: 80% of codons have A or T in the 3rd position. By Southern hybridisation, we located the *rpmH* gene to between 457 and 488 kbp on the *B.burgdorferi* physical map (8), close to the ribosomal RNA genes.

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Bb    MKRTYQPSRVKRNRKFGFRARMKTKGGRLILSRRRAKGRMKLTVSDEKKKY
      :::: ::: .:::: :::::: :: :: .: ::::::: ::::
Pm    MKRTFQPSVLKRNRNHGFRARMATKNGRQVLARRRAKGRARLTVSSK
      ::::::::::::: ::::::::::::::::::::::::::::::::
Ec    MKRTFQPSVLKRNRSHGFRARMATKNGRQVLARRRAKGRARLTVSK
      ::::::  .: : ::::::: :. :: .: :: : :.
Ml    MTKRTFQPNNRRRARKHGFRARMRTRAGRAILSARRGKNRAELSA
      :::: ::  . :: ::::::: :.
Mc    MKRTWQPSKLKHARVHGFRARMATK
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Figure 1. Alignment of sequences of ribosomal protein L34 from *B.burgdorferi* (Bb), *Proteus mirabilis* (Pm) (3), *Escherichia coli* (Ec) (4), *Micrococcus luteus* (Ml) (5) and a partial sequence from *Mycoplasma capricolum* (Mc) (6). Identical and homologous amino acids are highlighted by double and single dots, respectively. Accepted homologies are I-L-V-M-F, D-E, R-K, S-T.